

1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/536,087

DATE: 08/02/2001

TIME: 17:30:24

Input Set : A:\10287-051001.txt

Output Set: N:\CRF3\08022001\I536087.raw

ENTERED

4 <110> APPLICANT: Detmar, Michael J.
5 Streit, Michael
7 <120> TITLE OF INVENTION: THROMBOSPONDIN-2 AND USES THEREOF
9 <130> FILE REFERENCE: 10287-051001
11 <140> CURRENT APPLICATION NUMBER: 09/536,087
12 <141> CURRENT FILING DATE: 2000-03-24
14 <150> PRIOR APPLICATION NUMBER: 60/127,221
15 <151> PRIOR FILING DATE: 1999-03-31
17 <160> NUMBER OF SEQ ID NOS: 11
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3596
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (26)...(3541)
30 <400> SEQUENCE: 1

31	caggagctca gctgcaggag gcagg atg gtc tgg agg ctg gtc ctg ctg gct	52
32	Met Val Trp Arg Leu Val Leu Leu Ala	
33	1 5	
35	ctg tgg gtg tgg ccc agc acg caa gct ggt cac cag gac aaa gac acg	100
36	Leu Trp Val Trp Pro Ser Thr Gln Ala Gly His Gln Asp Lys Asp Thr	
37	10 15 20 25	
39	acc ttc gac ctt ttc agt atc agc aac atc aac cgc aag acc att ggc	148
40	Thr Phe Asp Leu Phe Ser Ile Ser Asn Ile Asn Arg Lys Thr Ile Gly	
41	30 35 40	
43	gcc aag cag ttc cgc ggg ccc gac ccc ggc gtg ccg gct tac cgc ttc	196
44	Ala Lys Gln Phe Arg Gly Pro Asp Pro Gly Val Pro Ala Tyr Arg Phe	
45	45 50 55	
47	gtg cgc ttt gac tac atc cca ccg gtg aac gca gat gac ctc agc aag	244
48	Val Arg Phe Asp Tyr Ile Pro Pro Val Asn Ala Asp Asp Leu Ser Lys	
49	60 65 70	
51	atc acc aag atc atg cgg cag aag gag ggc ttc ttc ctc acg gcc cag	292
52	Ile Thr Lys Ile Met Arg Gln Lys Glu Gly Phe Phe Leu Thr Ala Gln	
53	75 80 85	
55	ctc aag cag gac ggc aag tcc agg ggc acg ctg ttg gct ctg gag ggc	340
56	Leu Lys Gln Asp Gly Lys Ser Arg Gly Thr Leu Leu Ala Leu Glu Gly	
57	90 95 100 105	
59	ccc ggt ctc tcc cag agg cag ttc gag atc gtc tcc aat ggc ccc gcg	388
60	Pro Gly Leu Ser Gln Arg Gln Phe Glu Ile Val Ser Asn Gly Pro Ala	
61	110 115 120	
63	gac acg ctg gat ctc acc tac tgg att gac ggc acc cgg cat gtg gtc	436
64	Asp Thr Leu Asp Leu Thr Tyr Trp Ile Asp Gly Thr Arg His Val Val	
65	125 130 135	
67	tcc ctg gag gac gtc ggc ctg gct gac tcg cag tgg aag aac gtc acc	484
68	Ser Leu Glu Asp Val Gly Leu Ala Asp Ser Gln Trp Lys Asn Val Thr	

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69	140	145	150	
71	gtg cag gtg gct ggc gag acc tac agc ttg cac gtg ggc tgc gac ctc	532		
72	Val Gln Val Ala Gly Glu Thr Tyr Ser Leu His Val Gly Cys Asp Leu			
73	155	160	165	
75	ata gac agc ttc gct ctg gac gag ccc ttc tac gag cac ctg cag gcg	580		
76	Ile Asp Ser Phe Ala Leu Asp Glu Pro Phe Tyr Glu His Leu Gln Ala			
77	170	175	180	185
79	gaa aag agc cgg atg tac gtg gcc aaa ggc tct gcc aga gag agt cac	628		
80	Glu Lys Ser Arg Met Tyr Val Ala Lys Gly Ser Ala Arg Glu Ser His			
81	190	195	200	
83	ttc agg ggt ttg ctt cag aac gtc cac cta gtg ttt gaa aac tct gtg	676		
84	Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe Glu Asn Ser Val			
85	205	210	215	
87	gaa gat att cta agc aag aag ggt tgc cag caa ggc cag gga gct gag	724		
88	Glu Asp Ile Leu Ser Lys Lys Gly Cys Gln Gln Gly Gln Gly Ala Glu			
89	220	225	230	
91	atc aac gcc atc agt gag aac aca gag acg ctg cgc ctg ggt ccg cat	772		
92	Ile Asn Ala Ile Ser Glu Asn Thr Glu Thr Leu Arg Leu Gly Pro His			
93	235	240	245	
95	gtc acc acc gag tac gtg ggc ccc agc tca gag agg agg ccc gag gtg	820		
96	Val Thr Thr Glu Tyr Val Gly Pro Ser Ser Glu Arg Arg Pro Glu Val			
97	250	255	260	265
99	tgc gaa cgc tcg tgc gag gag ctg gga aac atg gtc cag gag ctc tcg	868		
100	Cys Glu Arg Ser Cys Glu Glu Leu Gly Asn Met Val Gln Glu Leu Ser			
101	270	275	280	
103	ggg ctc cac gtc ctc gtg aac cag ccc agc gag aac ctc aag aga gtg	916		
104	Gly Leu His Val Leu Val Asn Gln Pro Ser Glu Asn Leu Lys Arg Val			
105	285	290	295	
107	tcg aat gat aac cag ttt ctc tgg gag ctc att ggt ggc cct cct aag	964		
108	Ser Asn Asp Asn Gln Phe Leu Trp Glu Leu Ile Gly Gly Pro Pro Lys			
109	300	305	310	
111	aca agg aac atg tca gct tgc tgg cag gat ggc cgg ttc ttt gcg gaa	1012		
112	Thr Arg Asn Met Ser Ala Cys Trp Gln Asp Gly Arg Phe Phe Ala Glu			
113	315	320	325	
115	aat gaa acg tgg gtg gtg gac agc tgc acc acg tgt acc tgc aag aaa	1060		
116	Asn Glu Thr Trp Val Val Asp Ser Cys Thr Thr Cys Thr Cys Lys Lys			
117	330	335	340	345
119	ttt aaa acc att tgc cac caa atc acc tgc ccg cct gca acc tgc gcc	1108		
120	Phe Lys Thr Ile Cys His Gln Ile Thr Cys Pro Pro Ala Thr Cys Ala			
121	350	355	360	
123	agt cca tcc ttt gtg gaa ggc gaa tgc tgc cct tcc tgc ctc cac tcg	1156		
124	Ser Pro Ser Phe Val Glu Gly Glu Cys Cys Pro Ser Cys Leu His Ser			
125	365	370	375	
127	gtg gac ggt gag gag ggc tgg tct ccg tgg gca gag tgg acc cag tgc	1204		
128	Val Asp Gly Glu Glu Gly Trp Ser Pro Trp Ala Glu Trp Thr Gln Cys			
129	380	385	390	
131	tcc gtg acg tgt ggc tct ggg acc cag cag aga ggc cgg tcc tgt gac	1252		
132	Ser Val Thr Cys Gly Ser Gly Thr Gln Gln Arg Gly Arg Ser Cys Asp			
133	395	400	405	

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135	gtc	acc	agc	aac	acc	tgc	ttg	ggg	ccc	tcc	atc	cag	aca	cgg	gct	tgc	1300
136	Val	Thr	Ser	Asn	Thr	Cys	Leu	Gly	Pro	Ser	Ile	Gln	Thr	Arg	Ala	Cys	
137	410					415					420					425	
139	agt	ctg	agc	aag	tgt	gac	acc	cgc	atc	cgg	cag	gac	ggc	ggc	tgg	agc	1348
140	Ser	Leu	Ser	Lys	Cys	Asp	Thr	Arg	Ile	Arg	Gln	Asp	Gly	Gly	Trp	Ser	
141					430					435						440	
143	cac	tgg	tca	cct	tgg	tct	tca	tgc	tct	gtg	acc	tgt	gga	gtt	ggc	aat	1396
144	His	Trp	Ser	Pro	Trp	Ser	Ser	Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn	
145				445					450							455	
147	atc	aca	cgc	atc	cgt	ctc	tgc	aac	tcc	cca	gtg	ccc	cag	atg	ggg	ggc	1444
148	Ile	Thr	Arg	Ile	Arg	Leu	Cys	Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly	
149			460					465						470			
151	aag	aat	tgc	aaa	ggg	agt	ggc	cgg	gag	acc	aaa	gcc	tgc	cag	ggc	gcc	1492
152	Lys	Asn	Cys	Lys	Gly	Ser	Gly	Arg	Glu	Thr	Lys	Ala	Cys	Gln	Gly	Ala	
153		475						480						485			
155	cca	tgc	cca	atc	gat	ggc	cgc	tgg	agc	ccc	tgg	tcc	ccg	tgg	tcg	gcc	1540
156	Pro	Cys	Pro	Ile	Asp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	
157	490					495				500						505	
159	tgc	act	gtc	acc	tgt	gcc	ggt	ggg	atc	cgg	gag	cgc	acc	cgg	gtc	tgc	1588
160	Cys	Thr	Val	Thr	Cys	Ala	Gly	Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys	
161				510					515						520		
163	aac	agc	cct	gag	cct	cag	tac	gga	ggg	aag	gcc	tgc	gtg	ggg	gat	gtg	1636
164	Asn	Ser	Pro	Glu	Pro	Gln	Tyr	Gly	Gly	Lys	Ala	Cys	Val	Gly	Asp	Val	
165				525					530						535		
167	cag	gag	cgt	cag	atg	tgc	aac	aag	agg	agc	tgc	ccc	gtg	gat	ggc	tgt	1684
168	Gln	Glu	Arg	Gln	Met	Cys	Asn	Lys	Arg	Ser	Cys	Pro	Val	Asp	Gly	Cys	
169			540					545						550			
171	tta	tcc	aac	ccc	tgc	ttc	ccg	gga	gcc	cag	tgc	agc	agc	ttc	ccc	gat	1732
172	Leu	Ser	Asn	Pro	Cys	Phe	Pro	Gly	Ala	Gln	Cys	Ser	Ser	Phe	Pro	Asp	
173		555						560						565			
175	ggg	tcc	tgg	tca	tgc	ggc	tcc	tgc	cct	gtg	ggc	ttc	ttg	ggc	aat	ggc	1780
176	Gly	Ser	Trp	Ser	Cys	Gly	Ser	Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	
177	570					575						580				585	
179	acc	cac	tgt	gag	gac	ctg	gac	gag	tgt	gcc	ctg	gtc	ccc	gac	atc	tgc	1828
180	Thr	His	Cys	Glu	Asp	Leu	Asp	Glu	Cys	Ala	Leu	Val	Pro	Asp	Ile	Cys	
181					590					595						600	
183	ttc	tcc	acc	agc	aag	gtg	cct	cgc	tgt	gtc	aac	act	cag	cct	ggc	ttc	1876
184	Phe	Ser	Thr	Ser	Lys	Val	Pro	Arg	Cys	Val	Asn	Thr	Gln	Pro	Gly	Phe	
185				605					610						615		
187	cac	tgc	ctg	ccc	tgc	ccg	ccc	cga	tac	aga	ggg	aac	cag	ccc	gtc	ggg	1924
188	His	Cys	Leu	Pro	Cys	Pro	Pro	Arg	Tyr	Arg	Gly	Asn	Gln	Pro	Val	Gly	
189			620						625					630			
191	gtc	ggc	ctg	gaa	gca	gcc	aag	acg	gaa	aag	caa	gtg	tgt	gag	ccc	gaa	1972
192	Val	Gly	Leu	Glu	Ala	Ala	Lys	Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	
193		635						640						645			
195	aac	cca	tgc	aag	gac	aag	aca	cac	aac	tgc	cac	aag	cac	gcg	gag	tgc	2020
196	Asn	Pro	Cys	Lys	Asp	Lys	Thr	His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	
197	650					655						660				665	
199	atc	tac	ctg	ggc	cac	ttc	agc	gac	ccc	atg	tac	aag	tgc	gag	tgc	cag	2068

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200	Ile	Tyr	Leu	Gly	His	Phe	Ser	Asp	Pro	Met	Tyr	Lys	Cys	Glu	Cys	Gln	
201					670					675					680		
203	aca	ggc	tac	gcg	ggc	gac	ggg	ctc	atc	tgc	ggg	gag	gac	tcg	gac	ctg	2116
204	Thr	Gly	Tyr	Ala	Gly	Asp	Gly	Leu	Ile	Cys	Gly	Glu	Asp	Ser	Asp	Leu	
205				685					690					695			
207	gac	ggc	tgg	ccc	aac	ctc	aat	ctg	gtc	tgc	gcc	acc	aac	gcc	acc	tac	2164
208	Asp	Gly	Trp	Pro	Asn	Leu	Asn	Leu	Val	Cys	Ala	Thr	Asn	Ala	Thr	Tyr	
209			700					705					710				
211	cac	tgc	atc	aag	gat	aac	tgc	ccc	cat	ctg	cca	aat	tct	ggg	cag	gaa	2212
212	His	Cys	Ile	Lys	Asp	Asn	Cys	Pro	His	Leu	Pro	Asn	Ser	Gly	Gln	Glu	
213		715				720				725							
215	gac	ttt	gac	aag	gac	ggg	att	ggc	gat	gcc	tgt	gat	gat	gac	gat	gac	2260
216	Asp	Phe	Asp	Lys	Asp	Gly	Ile	Gly	Asp	Ala	Cys	Asp	Asp	Asp	Asp	Asp	
217	730				735					740					745		
219	aat	gac	ggt	gtg	acc	gat	gag	aag	gac	aac	tgc	cag	ctc	ctc	ttc	aat	2308
220	Asn	Asp	Gly	Val	Thr	Asp	Glu	Lys	Asp	Asn	Cys	Gln	Leu	Leu	Phe	Asn	
221				750					755					760			
223	ccc	cgc	cag	gct	gac	tat	gac	aag	gat	gag	gtt	ggg	gac	cgc	tgt	gac	2356
224	Pro	Arg	Gln	Ala	Asp	Tyr	Asp	Lys	Asp	Glu	Val	Gly	Asp	Arg	Cys	Asp	
225			765					770					775				
227	aac	tgc	cct	tac	gtg	cac	aac	cct	gcc	cag	atc	gac	aca	gac	aac	aat	2404
228	Asn	Cys	Pro	Tyr	Val	His	Asn	Pro	Ala	Gln	Ile	Asp	Thr	Asp	Asn	Asn	
229			780					785					790				
231	gga	gag	ggt	gac	gcc	tgc	tcc	gtg	gac	att	gat	ggg	gac	gat	gtc	ttc	2452
232	Gly	Glu	Gly	Asp	Ala	Cys	Ser	Val	Asp	Ile	Asp	Gly	Asp	Asp	Val	Phe	
233		795				800						805					
235	aat	gaa	cga	gac	aat	tgt	ccc	tac	gtc	tac	aac	act	gac	cag	agg	gac	2500
236	Asn	Glu	Arg	Asp	Asn	Cys	Pro	Tyr	Val	Tyr	Asn	Thr	Asp	Gln	Arg	Asp	
237	810				815					820					825		
239	acg	gat	ggt	gac	ggt	gtg	ggg	gat	cac	tgt	gac	aac	tgc	ccc	ctg	gtg	2548
240	Thr	Asp	Gly	Asp	Gly	Val	Gly	Asp	His	Cys	Asp	Asn	Cys	Pro	Leu	Val	
241				830					835					840			
243	cac	aac	cct	gac	cag	acc	gac	gtg	gac	aat	gac	ctt	gtt	ggg	gac	cag	2596
244	His	Asn	Pro	Asp	Gln	Thr	Asp	Val	Asp	Asn	Asp	Leu	Val	Gly	Asp	Gln	
245			845					850					855				
247	tgt	gac	aac	aac	gag	gac	ata	gat	gac	gac	ggc	cac	cag	aac	aac	cag	2644
248	Cys	Asp	Asn	Asn	Glu	Asp	Ile	Asp	Asp	Asp	Gly	His	Gln	Asn	Asn	Gln	
249			860					865					870				
251	gac	aac	tgc	ccc	tac	atc	tcc	aac	gcc	aac	cag	gct	gac	cat	gac	aga	2692
252	Asp	Asn	Cys	Pro	Tyr	Ile	Ser	Asn	Ala	Asn	Gln	Ala	Asp	His	Asp	Arg	
253		875				880						885					
255	gac	ggc	cag	ggc	gac	gcc	tgt	gac	cct	gat	gat	gac	aac	gat	ggc	gtc	2740
256	Asp	Gly	Gln	Gly	Asp	Ala	Cys	Asp	Pro	Asp	Asp	Asp	Asn	Asp	Gly	Val	
257	890				895					900					905		
259	ccc	gat	gac	agg	gac	aac	tgc	cgg	ctt	gtg	ttc	aac	cca	gac	cag	gag	2788
260	Pro	Asp	Asp	Arg	Asp	Asn	Cys	Arg	Leu	Val	Phe	Asn	Pro	Asp	Gln	Glu	
261				910					915						920		
263	gac	ttg	gac	ggt	gat	gga	cgg	ggt	gat	att	tgt	aaa	gat	gat	ttt	gac	2836
264	Asp	Leu	Asp	Gly	Asp	Gly	Arg	Gly	Asp	Ile	Cys	Lys	Asp	Asp	Phe	Asp	

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265          925          930          935
267 aat gac aac atc cca gat att gat gat gtg tgt cct gaa aac aat gcc      2884
268 Asn Asp Asn Ile Pro Asp Ile Asp Asp Val Cys Pro Glu Asn Asn Ala
269          940          945          950
271 atc agt gag aca gac ttc agg aac ttc cag atg gtc ccc ttg gat ccc      2932
272 Ile Ser Glu Thr Asp Phe Arg Asn Phe Gln Met Val Pro Leu Asp Pro
273          955          960          965
275 aaa ggg acc acc caa att gat ccc aac tgg gtc att cgc cat caa ggc      2980
276 Lys Gly Thr Thr Gln Ile Asp Pro Asn Trp Val Ile Arg His Gln Gly
277 970          975          980          985
279 aag gag ctg gtt cag aca gcc aac tcg gac ccc ggc atc gct gta ggt      3028
280 Lys Glu Leu Val Gln Thr Ala Asn Ser Asp Pro Gly Ile Ala Val Gly
281          990          995          1000
283 ttt gac gag ttt ggg tct gtg gac ttc agt ggc aca ttc tac gta aac      3076
284 Phe Asp Glu Phe Gly Ser Val Asp Phe Ser Gly Thr Phe Tyr Val Asn
285          1005          1010          1015
287 act gac cgg gac gac gac tat gcc ggc ttc gtc ttt ggt tac cag tca      3124
288 Thr Asp Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser
289          1020          1025          1030
291 agc agc cgc ttc tat gtg gtg atg tgg aag cag gtg acg cag acc tac      3172
292 Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Thr Tyr
293          1035          1040          1045
295 tgg gag gac cag ccc acg cgg gcc tat ggc tac tcc ggc gtg tcc ctc      3220
296 Trp Glu Asp Gln Pro Thr Arg Ala Tyr Gly Tyr Ser Gly Val Ser Leu
297 1050          1055          1060          1065
299 aag gtg gtg aac tcc acc acg ggg acg ggc gag cac ctg agg aac gcg      3268
300 Lys Val Val Asn Ser Thr Thr Gly Thr Gly Glu His Leu Arg Asn Ala
301          1070          1075          1080
303 ctg tgg cac acg ggg aac acg ccg ggg cag gtg cga acc tta tgg cac      3316
304 Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His
305          1085          1090          1095
307 gac ccc agg aac att ggc tgg aag gac tac acg gcc tat agg tgg cac      3364
308 Asp Pro Arg Asn Ile Gly Trp Lys Asp Tyr Thr Ala Tyr Arg Trp His
309          1100          1105          1110
311 ctg act cac agg ccc aag acc ggc tac atc aga gtc tta gtg cat gaa      3412
312 Leu Thr His Arg Pro Lys Thr Gly Tyr Ile Arg Val Leu Val His Glu
313          1115          1120          1125
315 gga aaa cag gtc atg gca gac tca gga cct atc tat gac caa acc tac      3460
316 Gly Lys Gln Val Met Ala Asp Ser Gly Pro Ile Tyr Asp Gln Thr Tyr
317 1130          1135          1140          1145
319 gct ggc ggg cgg ctg ggt cta ttt gtc ttc tct caa gaa atg gtc tat      3508
320 Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu Met Val Tyr
321          1150          1155          1160
323 ttc tca gac ctc aag tac gaa tgc aga gat att taaacaagat ttgctgcatt      3561
324 Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Ile
325          1165          1170
327 tccggcaatg ccctgtgcat gccatggtcc ctaga      3596
329 <210> SEQ ID NO: 2
330 <211> LENGTH: 1172

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